AMENDMENTS TO THE CLAIMS

The listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-48   (Canceled).

49.   (currently amended) A method performed in a computer of simulating a metabolic capability of an *in silico* strain of a microbe, comprising:

obtaining a plurality of DNA sequences comprising most of metabolic genes in a genome to produce an *in silico* representation of a microbe;

determining open reading frames of genes in said plurality of DNA sequences;

assigning a function to proteins encoded by said open reading frames by determining the homology of said open reading frames to gene sequences encoding proteins of known function;

determining which of said open reading frames correspond to metabolic genes by determining if the assigned function of said proteins is involved in cellular metabolism;

determining substrates, products and stoichiometry of the reaction for each of the gene products of said metabolic genes;

producing a genome specific stoichiometric matrix of said microbe produced from said substrates, products and stoichiometry;

determining a metabolic demand corresponding to a biomass composition of said microbe;

calculating uptake rates of metabolites of said microbe;

combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an *in silico* representation of said microbe;

incorporating a general linear programming problem to produce an *in silico* strain of said microbe;

performing a flux balance analysis on said *in silico* strain, and

providing a visual output to a user of said analysis that simulates a metabolic capability of said strain.

50.   (previously presented) The method of claim 49, wherein said microbe is *Escherichia coli.*

51.   (previously presented) The method of claim 49, wherein said genes involved in cellular metabolism comprise genes involved in central metabolism, amino acid metabolism, nucleotide metabolism, fatty acid metabolism, lipid metabolism, vitamin and cofactor biosynthesis, energy and redox generation or carbohydrate assimilation.

52.   (previously presented) The method of claim 49, wherein assigning a function comprises performing a homology search using the Basic Local Alignment Search Tool (BLAST).

Claims 53-55 (canceled).

56.   (previously presented) The method of claim 49, wherein said uptake rates are calculated by measuring the depletion of substrate from growth media of said microbe.

57.   (currently amended) A method performed in a computer for simulating a metabolic capability of an *in silico* strain of a microbe, comprising:

a)   providing a nucleotide sequence of a metabolic gene in the microbe;

b)   determining substrates, products and stoichiometry <u>of the reaction</u> for <u>the gene product of</u> said metabolic gene ~~product based on its assigned function~~;

c)   repeating steps a) and b) for most metabolic genes of said microbe to produce an *in silico* representation;

d)   producing a genome specific stoichiometric matrix produced from said substrates, products and stoichiometry of the metabolic ~~genes product~~ <u>gene products</u> in said microbe;

e)   determining a metabolic demand corresponding to a biomass composition of said microbe;

f)   calculating uptake rates of metabolites of said microbe<u>;</u> ~~, and~~

g)   combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an *in silico* representation of said microbe;

h)   incorporating a general linear programming problem to produce an *in silico* strain of said microbe;

i)   performing a flux balance analysis on said *in silico* strain; [[,]] and

j)   providing a visual output to a user of said analysis that simulates a metabolic capability of said strain.[[.]]

58.   (previously presented) The method of claim 57, wherein the microbe is *Escherichia coli.*

59.   (previously presented) The method of claim 57, wherein said metabolic gene is selected from the group consisting of: genes involved in central metabolism, amino acid metabolism, nucleotide metabolism, fatty acid metabolism, lipid metabolism, vitamin and cofactor biosynthesis, energy and redox generation and carbohydrate assimilation.

60.   (previously presented) The method of claim 57, wherein assigning a function comprises performing a homology search using the Basic Local Alignment Search Tool (BLAST).

Claim 61-63   (canceled).

64.   (previously presented) The method of claim 57, wherein said uptake rates are calculated by measuring the depletion of substrate from growth media of said microbe.

Claim 65-67   (canceled).